

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- 1
B
- (i) APPLICANT: Meissner, Paul S.
Coleman, Timothy A.
 - (ii) TITLE OF INVENTION: Human Cripin Growth Factor
 - (iii) NUMBER OF SEQUENCES: 7
 - (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Human Genome Sciences, Inc.
 - (B) STREET: 9410 Key West Avenue
 - (C) CITY: Rockville
 - (D) STATE: MD
 - (E) COUNTRY: USA
 - (F) ZIP: 20850
 - (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
 - (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 09/393,023
 - (B) FILING DATE: 09-SEP-1999
 - (C) CLASSIFICATION:
 - (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/471,371
 - (B) FILING DATE: 06-JUN-1995
 - (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Marks, Michelle S.
 - (B) REGISTRATION NUMBER: 41,971
 - (C) REFERENCE/DOCKET NUMBER: PF200D1
 - (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 301-309-8504
 - (B) TELEFAX: 301-309-8439



(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 672 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..672
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

| | |
|---|-----|
| ATG ACC TGG AGG CAC CAT GTC AGG CTT CTG TTT ACG GTC AGT TTG GCA | 48 |
| Met Thr Trp Arg His His Val Arg Leu Leu Phe Thr Val Ser Leu Ala | |
| 1 5 10 15 | |
| TTA CAG ATC ATC AAT TTG GGA AAC AGC TAT CAA AGA GAG AAA CAT AAC | 96 |
| Leu Gln Ile Ile Asn Leu Gly Asn Ser Tyr Gln Arg Glu Lys His Asn | |
| 20 25 30 | |
| GGC GGT AGA GGG GAA GTC ACC AAG GTT GCC ACT CAG AAG CAC CGA CAG | 144 |
| Gly Gly Arg Gly Glu Val Thr Lys Val Ala Thr Gln Lys His Arg Gln | |
| 35 40 45 | |
| TCA CCG CTT AAC TGG ACC TCC AGT CAT TTC GGA GAG GTG ACT GGG AGC | 192 |
| Ser Pro Leu Asn Trp Thr Ser Ser His Phe Gly Glu Val Thr Gly Ser | |
| 50 55 60 | |
| GCC GAG GGC TGG GGG CCG GAG GAG CCG CTC CCC TAC TCC CGG GCT TTC | 240 |
| Ala Glu Gly Trp Gly Pro Glu Glu Pro Leu Pro Tyr Ser Arg Ala Phe | |
| 65 70 75 80 | |
| GGA GAG GGT GCG TCC GCG CGG CCG CGC TGC TGC AGG AAC GGC GGT ACC | 288 |
| Gly Glu Gly Ala Ser Ala Arg Pro Arg Cys Cys Arg Asn Gly Gly Thr | |
| 85 90 95 | |
| TGC GTG CTG GGC AGC TTC TGC GTG TGC CCG GCC CAC TTC ACC GGC CGC | 336 |
| Cys Val Leu Gly Ser Phe Cys Val Cys Pro Ala His Phe Thr Gly Arg | |
| 100 105 110 | |
| TAC TGC GAG CAT GAC CAG AGG CGC AGT GAA TGC GGC GCC CTG GAG CAC | 384 |
| Tyr Cys Glu His Asp Gln Arg Arg Ser Glu Cys Gly Ala Leu Glu His | |
| 115 120 125 | |
| GGA GCC TGG ACC CTC CGC GCC TGC CAC CTC TGC AGG TGC ATC TTC GGG | 432 |
| Gly Ala Trp Thr Leu Arg Ala Cys His Leu Cys Arg Cys Ile Phe Gly | |
| 130 135 140 | |
| GCC CTG CAC TGC CTC CCC CTC CAG ACG CCT GAC CGC TGT GAC CCG AAA | 480 |
| Ala Leu His Cys Leu Pro Leu Gln Thr Pro Asp Arg Cys Asp Pro Lys | |
| 145 150 155 160 | |
| GAC TTC CTG GCC TCC CAC GCT CAC GGG CCG AGC GCC GGG GGC GCG CCC | 528 |
| Asp Phe Leu Ala Ser His Ala His Gly Pro Ser Ala Gly Gly Ala Pro | |
| 165 170 175 | |
| AGC CTG CTA CTC TTG CTG CCC TGC GCA CTC CTG CAC CGC CTC CTG CGC | 576 |
| Ser Leu Leu Leu Leu Pro Cys Ala Leu Leu His Arg Leu Leu Arg | |
| 180 185 190 | |
| CCG GAT GCG CCC GCG CAC CCT CGG TCC CTG GTC CCT TCC GTC CTC CAG | 624 |
| Pro Asp Ala Pro Ala His Pro Arg Ser Leu Val Pro Ser Val Leu Gln | |
| 195 200 205 | |
| CGG GAG CGG CGC CCC TGC GGA AGG CCG GGA CTT GGG CAT CGC CTT TAA | 672 |
| Arg Glu Arg Arg Pro Cys Gly Arg Pro Gly Leu Gly His Arg Leu * | |
| 210 215 220 | |

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 224 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Thr Trp Arg His His Val Arg Leu Leu Phe Thr Val Ser Leu Ala
1 5 10 15

Leu Gln Ile Ile Asn Leu Gly Asn Ser Tyr Gln Arg Glu Lys His Asn
20 25 30

Gly Gly Arg Gly Glu Val Thr Lys Val Ala Thr Gln Lys His Arg Gln
35 40 45

Ser Pro Leu Asn Trp Thr Ser Ser His Phe Gly Glu Val Thr Gly Ser
50 55 60

Ala Glu Gly Trp Gly Pro Glu Glu Pro Leu Pro Tyr Ser Arg Ala Phe
65 70 75 80

Gly Glu Gly Ala Ser Ala Arg Pro Arg Cys Cys Arg Asn Gly Gly Thr
85 90 95

Cys Val Leu Gly Ser Phe Cys Val Cys Pro Ala His Phe Thr Gly Arg
100 105 110

Tyr Cys Glu His Asp Gln Arg Arg Ser Glu Cys Gly Ala Leu Glu His
115 120 125

Gly Ala Trp Thr Leu Arg Ala Cys His Leu Cys Arg Cys Ile Phe Gly
130 135 140

Ala Leu His Cys Leu Pro Leu Gln Thr Pro Asp Arg Cys Asp Pro Lys
145 150 155 160

Asp Phe Leu Ala Ser His Ala His Gly Pro Ser Ala Gly Gly Ala Pro
165 170 175

Ser Leu Leu Leu Leu Leu Pro Cys Ala Leu Leu His Arg Leu Leu Arg
180 185 190

Pro Asp Ala Pro Ala His Pro Arg Ser Leu Val Pro Ser Val Leu Gln
195 200 205

Arg Glu Arg Arg Pro Cys Gly Arg Pro Gly Leu Gly His Arg Leu *

210 215 220

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cont.

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ACTCTTGGAT CCAATTGGG AACAGCTAT CAAAGA

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 42 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TACAACTCTA GACTATTATT TACAACATAG AAAATTAAAG GC

42

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ACTCTTGGAT CCGCCATCAT GACCTGGAGG CACCAT

36

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 42 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TACAACTCTA GACTATTATT TACAACATAG AAAATTAAAG GC

42

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 174 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | His | Ala | Ala | Ile | Ser | Lys | Val | Phe | Glu | Leu | Gly | Leu | Val | Ala | Gly |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Leu | Gly | His | Gln | Glu | Phe | Ala | Arg | Pro | Ser | Arg | Gly | Tyr | Leu | Ala | Phe |
| | | | 20 | | | | | 25 | | | | | 30 | | |

B1
cont

Arg Asp Asp Ser Ile Trp Pro Gln Glu Glu Pro Ala Ile Arg Pro Arg
 35 40 45
 Ser Ser Gln Arg Val Pro Pro Met Gly Ile Gln His Ser Lys Glu Leu
 50 55 60
 Asn Arg Thr Cys Cys Leu Asn Gly Gly Thr Cys Met Leu Gly Ser Phe
 65 70 75 80
 Cys Ala Cys Pro Pro Ser Phe Tyr Gly Arg Asn Cys Glu His Asp Val
 85 90 95
 Arg Lys Glu Asn Cys Gly Ser Val Pro His Asp Thr Trp Leu Pro Lys
 100 105 110
 Lys Cys Ser Leu Cys Lys Cys Trp His Gly Gln Leu Arg Cys Phe Pro
 115 120 125
 Gln Ala Phe Leu Pro Gly Cys Asp Gly Leu Val Met Asp Glu His Leu
 130 135 140
 Val Ala Ser Arg Thr Pro Glu Leu Pro Pro Ser Ala Arg Thr Thr Thr
 145 150 155 160
 Phe Leu Met Val Gly Ile Cys Leu Ser Ile Gln Ser Tyr Tyr
 165 170

B!
 (incl.)